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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:18:03 ; Search time 1569.94 Seconds
(without alignments)
12007.805 Million cell updates/sec

Title: US-09-807-933B-10

Perfect score: 1164
Sequence: 1 atgaagtcacacgttcgtcat.....caggttcggaagaagaa 1164

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_ges:*
18: em_ges_hum:*
19: em_ges_inv:*
20: em_ges_pln:*
21: em_ges_vrt:*
22: em_ges_fun:*
23: em_ges_mam:*
24: em_ges_mus:*
25: em_ges_other:*
26: em_ges_pro:*
27: em_ges_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	173	14.9	691	10	BE585661 EST#6PSP6
2	122.2	10.5	450	13	BI200729 BI100568.r
3	111	9.5	444	13	BI190695 BI131058.r
4	104.4	9.0	426	13	BI187295 BI181118.r
5	81.2	7.0	215	13	BI190568 BI190568
6	73.6	6.3	989	17	CNS02HMA4 AT197365 Tetradon

7	72	6.2	494	17	PR0048073
8	70.8	6.1	350	17 <td>BH879665</td>	BH879665
9	70.6	6.1	450	17 <td>PR0025663</td>	PR0025663
10	70.6	6.1	501	17 <td>FR0048173</td>	FR0048173
11	70	6.0	914	17 <td>AZ205202</td>	AZ205202
12	69.6	6.0	933	17 <td>AZ204694</td>	AZ204694
13	67.8	5.8	788	17 <td>AZ183942</td>	AZ183942
14	67.2	5.8	627	17 <td>BH179321</td>	BH179321
15	67.2	5.8	627	17 <td>CNS071FL</td>	CNS071FL
16	66	5.7	735	17 <td>CNS04NSM</td>	CNS04NSM
17	65.8	5.7	335	10 <td>AW275677</td>	AW275677
18	65.8	5.7	619	17 <td>FR0047601</td>	FR0047601
19	65.6	5.6	570	17 <td>AZ149014</td>	AZ149014
20	65.2	5.6	530	17 <td>AZ166409</td>	AZ166409
21	64.8	5.5	392	17 <td>PR0048008</td>	PR0048008
22	64.2	5.5	331	17 <td>BH881398</td>	BH881398
23	64	5.5	500	17 <td>B67199</td>	B67199
24	63.8	5.5	354	17 <td>AQ935615</td>	AQ935615
25	63.4	5.4	250	17 <td>BH878991</td>	BH878991
26	63.2	5.4	824	17 <td>AZ185454</td>	AZ185454
27	62.8	5.4	773	17 <td>CNS01VTG</td>	CNS01VTG
28	62.6	5.4	522	13 <td>B1783235</td>	B1783235
29	62.6	5.4	621	17 <td>AZ164800</td>	AZ164800
30	62.2	5.3	358	17 <td>BH777606</td>	BH777606
31	62.2	5.3	580	17 <td>BH763893</td>	BH763893
32	62	5.3	177	17 <td>BH881173</td>	BH881173
33	62	5.3	204	17 <td>BH882682</td>	BH882682
34	62	5.3	230	17 <td>BH869848</td>	BH869848
35	62	5.3	510	13 <td>B0374789</td>	B0374789
36	62	5.3	619	17 <td>FR0006944</td>	FR0006944
37	62	5.3	810	17 <td>AZ199472</td>	AZ199472
38	61.8	5.3	218	17 <td>BH875125</td>	BH875125
39	61.2	5.3	796	17 <td>AZ186967</td>	AZ186967
40	60.6	5.2	454	17 <td>AZ178507</td>	AZ178507
41	60.2	5.2	976	17 <td>CNS01FBX</td>	CNS01FBX
42	60	5.2	558	17 <td>AZ146816</td>	AZ146816
43	59.8	5.1	539	9 <td>AT002510</td>	AT002510
44	59.6	5.1	485	13 <td>BJ370491</td>	BJ370491
45	59.4	5.1	196	17 <td>PR0047508</td>	PR0047508

ALIGNMENTS

RESULT 1
BE585661
LOCUS
DEFINITION
CDNA library Trifolium aestivum CDNA clone EST#6PSP6_D02_d2_014
ACCESSION
BE585661
VERSION
BE585661.1
KEYWORDS
SOURCE
ORGANISM
broad wheat.
Trifolium aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
; Triciteae; Tricicum.
1 (bases 1 to 691)
Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.
The structure and function of the expressed portion of the wheat
genomes - Kansas State University. Fusarium graminearum infected
spike cDNA library
Unpublished (2000)
Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@alfalfa.ksu.edu
Sequence have been trimmed to remove vector sequence and low

JOURNAL
COMMENT

quality sequence with phred score less than 20
 Seg primer: SP6.
 Location/Qualifiers

FEATURES
 source

1. 691
 /organism="Triticum aestivum"
 /cultivar="Sumai3"
 /db_xref="taxon:4565"
 /clone="EST#SPSP6 D02 d2 014"
 /clone_lib="KSU wheat Fusarium graminearum infected spike
 cDNA library"
 /tissue_type="Spike"
 /dev_stage="Adult plant"
 /lab_host="E. coli JM109"
 /note="Vector: pGEM-T easy; Site 1: SacII; Site 2: SpeI;
 plants were grown in the greenhouse. Spikes were sprayed
 with Fusarium graminearum (at what stage). Total RNA, and
 poly(A) RNA were prepared from infected spikes. cDNA was
 prepared using the SmartTM PCR cDNA synthesis kit from
 Clontech. cDNA was cloned into the pGEM-T easy vector
 from Promega."

BASE COUNT 135 a 196 c 163 g 197 t

ORIGIN

Query Match 14.9%; Score 173; DB 10; Length 691;
 Best Local Similarity 63.8%; Pred. No. 2.4e-39;
 Matches 279; Conservative 0; Mismatches 155; Indels 3; Gaps 1;

547 TCTGGAGTGGTTCACAACTGTTATTTGGATTGTTAAAGCTTCTTGAGCTGAGCT 606
 168 TCTGGAGTGGTTCACAACTGTTATTTGGATTGTTAAAGCTTCTTGAGCTGAGCT 227
 607 GGAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
 228 GGCAAGGCAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 287
 667 GATGCCAATGCTCAAGTGGTGT--AACGGTGTATGGTTTCATGTATACAAAC 723
 288 AACCTGAACGCGCTCAACGCTGTGAGAGTGGTGTGCTGCTGCTGCTGCTGCTGCT 347
 724 CAACCTTGGGCTGCTCAATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
 348 TCCCTTGGGCTGCTCAACGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 407
 784 TCCAAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
 408 GGCACTAGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 467
 844 TCTGGAAGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
 468 AAGGGAAGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 527
 904 TTGATTTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 963
 528 TTTTACCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 587
 964 GCGGCTCCCAATGATG 980
 588 GGCAAGCCCTCGGTG 604

RESULT 2
 BI200729 450 bp mRNA linear EST 10-JUL-2001
 LOCUS o1f05fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 DEFINITION library Fusarium sporotrichioides cDNA clone o1f05fs 5', mRNA
 sequence.

ACCESSION BI200729
 VERSION BI200729.1
 KEYWORDS GI:14666701
 SOURCE EST
 ORGANISM Fusarium sporotrichioides
 Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 450)
 AUTHORS Ren Q., Tag A., Papiou A., Lai H., Kupfer C., Peterson A., Beremand
 M., and Roe B.
 TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)
 COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 633 5e-66 94|1170140|sp|P45699 PUFATIVE ENDOGLUCANASE TYPE
 KRECURSOR (EN
 Seq primer: T3
 High quality sequence step: 440.

FEATURES

source

Location/Qualifiers
 1. 450
 /organism="Fusarium sporotrichioides"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="o1f05fs"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
 cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
 ; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 90 a 125 c 102 g 133 t

ORIGIN

Query Match 10.5%; Score 122.2; DB 13; Length 450;
 Best Local Similarity 63.6%; Pred. No. 1.5e-24;
 Matches 203; Conservative 0; Mismatches 113; Indels 3; Gaps 1;

547 TCTGGAGTGGTTCACAACTGTTATTTGGATTGTTAAAGCTTCTTGAGCTGAGCT 606
 132 TCTGGAGTGGTTCACAACTGTTATTTGGATTGTTAAAGCTTCTTGAGCTGAGCT 191
 607 GGAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
 192 GGCAAGGCAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 251
 667 GATGCCAATGCTCAAGTGGTGTAA---CGTGTATGTTTCAATGTTTAAACAAC 723
 252 AACCTGAACGCGCTCAACGCTGTGAGAGTGGTGTGCTGCTGCTGCTGCTGCTGCT 311
 724 CAACCTTGGGCTGCTCAATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
 312 TCCCTTGGGCTGCTCAACGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371
 784 TCCAAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
 372 GGTATGAGGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
 844 TCTGGAAGAAGATGCTG 862
 432 AAGGCAAGAAGATGATG 450

RESULT 3
 BI190695 444 bp mRNA linear EST 10-JUL-2001
 LOCUS i3g10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 DEFINITION library Fusarium sporotrichioides cDNA clone i3g10fs 5', mRNA
 sequence.

ACCESSION BI190695
 VERSION BI190695.1
 KEYWORDS GI:14664374
 SOURCE EST
 ORGANISM Fusarium sporotrichioides
 Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

REFERENCE	TITLE	JOURNAL	COMMENT
1 (bases 1 to 444)	Hypocretales; mitosporic Hypocretales; Fusarium.		
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M., and Roe, B.	Analysis of a Fusarium sporotrichioides EST database		
Published (2001)	Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu		
Department of Chemistry and Biochemistry	Advanced Center for Genome Technology, University of Oklahoma		
620 Parrington Oval, Norman, OK 73019, USA	Tel: 405 325 4912		
Fax: 405 325 7762	Email: broe@ou.edu		
Contact Dr. Marian Beremand regarding clone availability Included	is the best homolog from a blastx search of Genbank nr 04-09-01		
576 3e-59 g1.1170140 sp P45699 PUTATIVE ENDOGLUCANASE TYPE	KPRECURSOR (NF)		
Seq primer: T3.	Location/Qualifiers		
1. 444	/organism="Fusarium sporotrichioides"		
/strain="T3 10"	/db_xref="taxon:5514"		
/clone="13g10f6"	/clone_lib="Fusarium sporotrichioides T3 10 overexpressed		
CDNA library"	/note="vector: pBluescript SK-, site 1: EcoRI; site 2:		
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript	; 3' end of cDNA cloned into XhoI site of pBluescript"		
BASE COUNT	85 a 127 c 92 g 140 t		
ORIGIN			
Query Match	9.5%; Score 111; DB 13; Length 444;		
Best Local Similarity	64.1%; Pred. No. 2.9e-21;		
Matches 184; Conservative	0; Mismatches 100; Indels 3; Gaps 1;		
Oy	547 TCTGGCAGTGGTTCACACACTGCTTATTTGGATTTGTCTAAAGCTTCTGCAGCTGGCT	606	
Db	158 TCTGGAAATGGCCACTCTACTCGATACGAGGACTGCTGCAAC3CCTTCTGCTTGGAGC	217	
Oy	607 GGAAAGCTTCGTCACATCGTCCGTTGACACCTGTCCTCCAAATGGATCTTTATTA	666	
Db	218 GGCAGGCTTAAGTACGAGCCCTGCTCTGACTTGTGCAADAAATTAACCTATCACT	277	
Oy	667 GATGCCATGCTCAAGTGGTTGTAA---CGGTGATAGCTTTCAATGTAAACAAC	723	
Db	278 AACCGAAGCGTCAACGTTGAGGGTGTGTTCTGCTATGCTTGACCAACTAC	337	
Oy	724 CAACCTGGGCTGCATGATGATGAGTCCCTTAACGGTTTCGCTGCTCTATTGCTGC	783	
Db	338 TCCCGTGGGCTGTCACAGACACTTCTTAACGGTTTCGCTGCTACCAAGCTTGGGT	397	
Oy	784 TCCAACGAGCTGATGCTGTTGCGCTGATGATGAATGACCTTAC	830	
Db	398 GGTATGAGGCGACGCTGGTGGCTGCTGCTATGCTTCACCTTAC	444	
RESULT 4			
LOCUS	B1187295	426 bp	mRNA linear EST 10-JUL-2001
DEFINITION	alb1ife.v1 Fusarium sporotrichioides T3 10 overexpressed cDNA		
library Fusarium sporotrichioides cDNA clone alb1ife 5', mRNA	sequence.		
ACCESSION	B1187295		
VERSION	B1187295.1	GI:14660974	
KEYWORDS	EST.		
SOURCE	Fusarium sporotrichioides.		
ORGANISM	Fusarium sporotrichioides.		
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
AUTHORS	Hypocretales; mitosporic Hypocretales; Fusarium.		
	1 (bases 1 to 426)		
	Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand,		
	M., and Roe, B.		

TITLE	COMMENT	FEATURES	BASE COUNT	ORIGIN
Analysis of a Fusarium sporotrichioides EST database	Unpublished (2001)			
Other ESTs: alh11f, f1	Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu			
Department of Chemistry and Biochemistry	Advanced Center for Genome Technology, University of Oklahoma			
620 Parrington Oval, Norman, OK 73019, USA	Tel: 405 325 4912			
Fax: 405 325 7762	Email: broe@ou.edu			
Contract Dr. Marian Beremand regarding clone availability included	is the best homolog from a blastx search of Genbank nr 04-09-01			
565 56-58 g 11170140 sp P45699 PUTATIVE ENDOGLUCANASE TYPE	KREPCR5OR (EN			
Seq primer: T3	Location/Qualifiers			
High quality sequence stop: 338.	1. 426			
	/organism="Fusarium sporotrichioides"			
	/strain="Tri 10"			
	/db_xref="taxon:5514"			
	/clone="alh11f8"			
	/cdna_lib="Fusarium sporotrichioides Tri 10 overexpressed			
	/cdna_library"			
	/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:			
	XhoI; 5' end of CDNA cloned into EcoRI site of pBluescript			
	; 3' end of CDNA cloned into XhoI site of pBluescript"			
82 a 119 c 91 g 134 t				
Query Match 9.0%; Score 104.4; DB 13; Length 426;				
Best Local Similarity 63.9%; Pred. No. 2.5e-19;				
Matches 175; Conservative 0; Mismatches 96; Indels 3; Gaps 1;				
OY TCTGGAGTGGTTCACAACTCGTTATGGATTGTGTAAAGCTTCTTGACGCTGGCCT	606			
148 TCTGGAAATGGCCACTTACTCGATCTGGAGCTCTGCAGACCTTCTTGCGAGC	207			
607 GGAAAGCTTGTCTACTGTGCTCTGTGACACCTGTGCCTCAATGATCTCTTTATTA	666			
208 GGCAAGGCTAAAGTCAGAGGCCCTCGTCTGTGACCAACAAAGATTAACCTATCACT	267			
OY GATGCCAATGCTCAAAGTGGTTGA--CGGTGTATGTTTCATGATGTGAACAAAC	723			
268 AACCTGAACGCTGCACACGCTTGTGAGAGGTGTGTCTGCTTATGCTTGACCACTAC	327			
OY CAACCTGGGGCTGCATGATGATGACCTGGCTTACGGTTTGGCTGCTCATTTGCTGGC	783			
328 TCCCGTGGGGCTGCACAGACGACCTTGTACGTTTGGCTGCTTACCAAGCTTGGCT	387			
OY TCCACGAGCTGATGTGTTTGTGGCTGTATG	817			
388 GGTAGTAGGCGACACTGTGTCTGTGCTTGTATG	421			
RESULT 5	215 bp	linear	EST 10-JUN-2001	
LOCUS B1190568	12el11f5.r1	Fusarium sporotrichioides Tri 10 overexpressed CDNA		
DEFINITION library	Fusarium sporotrichioides CDNA clone 12el11f5 5', mRNA			
ACCESSION B1190568	GI:14664247			
VERSION B1190568				
KEYWORDS EST.				
SOURCE	Fusarium sporotrichioides.			
ORGANISM	Fusarium sporotrichioides			
REFERENCE	Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
AUTHORS	Hypocreales; mitosporic Hypocreales; Fusarium.			
TITLE	1 (bases 1 to 215)			
JOURNAL	Ren,O., Tag,A., Peglow,A., Lai,H., Kuper,C., Peterson,A., Beremand			
	M. and Roe,B.			
	Analysis of a Fusarium sporotrichioides EST database			
	Unpublished (2001)			

sequence Location/Qualifiers

FEATURES
source 1. .450
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone="154E17a12"
/clone_1lb="cosmid 154E17"

BASE COUNT 96 a 140 c 64 g 144 t 6 others

Query Match 6.1%; Score 70.6; DB 17; Length 450;
Best Local Similarity 50.4%; Pred. No. 2.2e-09; Indels 0; Gaps 0;
Matches 172; Conservative 0; Mismatches 169;

ORIGIN
Query Match 6.1%; Score 70.6; DB 17; Length 450;
Best Local Similarity 50.4%; Pred. No. 2.2e-09; Indels 0; Gaps 0;
Matches 172; Conservative 0; Mismatches 169;

365 CTACAGACCAAGAGACATCTTCCAGACATCTTACCAAGGCTACTGCTA 424
78 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 137
425 CTGTCCACCAAGACAGACATCTTCCAGACATCTTACCAAGGCTACTGCTA 484
138 CTGTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 197
485 CTGCGCGCTCTTCTTCTTCCAGACATCTTCCAGACATCTTCCAGGCTA 544
198 CTGCTGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTA 257
545 AATCTGACGAGTTCACCACTGTTATGAGATTGTTGAAGCTTCTTGACGCTGC 604
258 CTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 317
605 CTGGAAGCTTCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 664
318 CTATTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTGCTG 377
665 TAGATGCCAATGCTCAAGTGGTGTGTAAGGTGTAATGCT 705
378 CTGCTACTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTGCT 418

RESULT 10
FR0048173 501 bp DNA linear GSS 05-JAN-2001
LOCUS
DEFINITION Fugu rubripes GSS sequence, clone 264E22cA9, genomic survey

ACCESSION AL444958.1 GI:12053458
VERSION AL444958.1
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes.
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.

REFERENCE 1 (bases 1 to 501)

AUTHORS Clark, M.S.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB, UK Email:
biohelp@hgm.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS

COMMENT
DESCR: One pass dye-terminator sequencing of BAC (pBeloBAC11) cloned
genomic sequence
The BACs can be obtained from <http://www.incyte.com>.

FEATURES
source 1. .501
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone="264E22cA9"
/clone_1lb="BAC 264E22"

BASE COUNT 132 a 161 c 35 g 173 t

ORIGIN

Query Match 6.1%; Score 70.6; DB 17; Length 501;
Best Local Similarity 50.1%; Pred. No. 2.4e-09;
Matches 175; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

ORIGIN
Query Match 6.1%; Score 70.6; DB 17; Length 501;
Best Local Similarity 50.1%; Pred. No. 2.4e-09;
Matches 175; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

354 TGCTGTAGAGCTAGACAGACCAAGACATCTTACCAAGACATCTTACCAAGGCTA 413
140 TGCTTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 199
414 GGTACTGCTACTGCTTCAAGCAAGACAGTAAACCAAGACATCTTACCAAGGCTA 473
200 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 259
474 GACTAGACATCTGCGCTGCTTCTTCACTCTTCTTCTTCTGCTGTTACAGGCTA 533
260 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 319
534 CTGCGCGTAAATCTGAGATGCTTCCAGACATCTTCCAGACATCTTCCAGGCTT 593
320 TTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 379
594 TTGACGCTGCGCTGGAAGCTTCTGCTACTGCTGCTGCTGCTGCTGCTGCTA 653
380 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 439
654 TATCTCTTATTAAGTCAATGCTCAAGGTTGTAAGGTTAAT 702
440 TGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTA 488

RESULT 11
AZ205202 914 bp DNA linear GSS 31-AUG-2000
LOCUS
DEFINITION SP 0100 A2 G12 SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=100 Col=24 Row=M, DNA sequence.

ACCESSION AZ205202.1 GI:8400122
VERSION AZ205202.1
KEYWORDS Strongylocentrotus purpuratus.
SOURCE Strongylocentrotus purpuratus.
ORGANISM Strongylocentrotus purpuratus.
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 914)

AUTHORS Cameron, R.A., Mahitres, G., Rast, J.P., Martinez, P., Bondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Eitensohn, C.A., Lehnach, H., Britten, R.J., Davidson, E.H. and Hood, L.
TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
MEDLINE 20402566
CONTACT: Cameron, RA, Davidson, EH, Hood, L
DIVISION of Biology 156-29
CALIFORNIA INSTITUTE OF TECHNOLOGY
PASADENA CALIFORNIA 91125, USA
TEL: (626) 395-8421
FAX: (626) 793-3047
EMAIL: acameron@caltech.edu
PLATE: 100 ROW: M COLUMN: 24
SEQ PRIMER: SP6
CLAS: BAC ends
HIGH QUALITY SEQUENCE STOP: 914.

FEATURES
source 1. .914
/organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/clone="Plate=100 Col=24 Row=M"
/clone_1lb="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACs; 6; BAC clones in E-Coli

BASE COUNT 210 a 208 c 107 g 387 t 2 others
 ORIGIN DH10B"

Query Match 6.0%; Score 70; DB 17; Length 914;
 Best Local Similarity 48.7%; Pred. No. 5.6e-09;
 Matches 190; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

QY 346 AGTACATGCTGTGTAACGTAGACGACCAAGACATCTACCAAGATCTACTACC 405
 DB 169 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 228
 QY 406 ACCGCAAGGCTACTGTACTGTACCAACCAAGCAAGTACCAAGCACTACTACTACT 465
 DB 229 ACCACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 288
 QY 466 ACTACCAAGTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 525
 DB 289 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 348
 QY 526 AAGTCACTCTGCGGTAATCTGAGAGTGTCCCAACTGTTATTTGGATTGTGT 585
 DB 349 ACTGTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 408
 QY 586 AAGCTTCTTGCGCTGCGCTGGAAGCTTGTCTGCTGCTGCTGCTGCTGCTGCTG 645
 DB 409 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 468
 QY 646 TCCATGCTACTCTTTTATTAGATGCCAATGCTCAAGTGTGAACGGTGTAAATG 705
 DB 469 ACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 528
 QY 706 TTCTATGTGTACCAACCAACCACTGTGGCT 735
 DB 529 TTGTATATATATATATATATATATGCTGAGT 558

RESULT 12
 LOCUS AZ204694 933 bp DNA linear GSS 31-AUG-2000
 DEFINITION SP 0100. A1 G12. SP68 Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=100 Col=23 Row=M, DNA sequence.

ACCESSION AZ204694.1 GI:8399614
 VERSION GSS.
 KEYWORDS Strongylocentrotus purpuratus.
 ORGANISM Strongylocentrotus purpuratus
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinocida;
 Strongylocentrotidae; Strongylocentrotus.

REFERENCE
 AUTHORS

TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 MEDLINE 20402566
 COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
 Division of Biology 156-29
 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu
 Plate: 100 row: M column: 23
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 933.
 Location/Qualifiers
 1..933

FEATURES
 Source

/organism="Strongylocentrotus purpuratus"
 /db_xref="taxon:7668"
 /clone="Plate=100 Col=23 Row=M"
 /clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli DH10B"

BASE COUNT 226 a 235 c 156 g 316 t
 ORIGIN

Query Match 6.0%; Score 69.6; DB 17; Length 933;
 Best Local Similarity 48.9%; Pred. No. 7.4e-09;
 Matches 186; Conservative 0; Mismatches 194; Indels 0; Gaps 0;

QY 336 CGGATCCACAGTACAAAGCTGTGTAACGCTAGACGACCAAGACATCTACCAAG 395
 DB 110 CGGATCCACGCGCAATCTACTACTACTACTACTACTACTACTACTACTACTACT 169
 QY 396 ATCTATACACCGCCAGGCTACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 455
 DB 170 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 229
 QY 456 TACCAAGACACTACCAAGACTAGACACTGCGGCTGCTTACTTCCACTCTTCTC 515
 DB 230 CACCACTACTACTACTTCCACTATTTACTACTACTACTACTACTACTACTACTACT 289
 QY 516 TGTGTGTACAGGTATCTGCGGTAATGTGCAAGTGTCCCAACTGTTATTG 575
 DB 290 TACTACTTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTT 349
 QY 576 GGAATGTGTAAGCTTCTGAGCTGCGCTGGAAGCTTGTGCTGCTGCTGCTGCTG 635
 DB 350 TGTATATATATCTACTACTTCTACTACTACTACTACTACTACTACTACTACTACT 409
 QY 636 CACCTGCTCCCAATGATCTTTTATTAGATGCCAATGCTCAAGTGTGTAAACGG 695
 DB 410 TACTACTACTACTACTTACCACTACTACTACTACTACTACTACTACTACTACTACT 469
 QY 696 TGTATGTTGTTGATGTGA 715
 DB 470 TATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 489

RESULT 13
 LOCUS AZ183942 788 bp DNA linear GSS 30-AUG-2000
 DEFINITION SP 1002. A1 H11. SP6 Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1002 Col=21 Row=O, DNA sequence.

ACCESSION AZ183942.1 GI:8356317
 VERSION GSS.
 KEYWORDS Strongylocentrotus purpuratus.
 ORGANISM Strongylocentrotus purpuratus
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinocida;
 Strongylocentrotidae; Strongylocentrotus.

REFERENCE
 AUTHORS

TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 MEDLINE 20402566
 COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
 Division of Biology 156-29
 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu

FEATURES
 Source

Plate: 1002 row: 0 column: 21
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 788.
 Location/Qualifiers

FEATURES

Source

1. 788
 /organism="Strongylocentrotus purpuratus"
 /db_xref="taxon:7668"
 /clone="plate:1002 Col=21 Row=0"
 /clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli DH10B"

BASE COUNT 248 a 183 c 98 g 259 t

ORIGIN

Query Match 5.8%; Score 67.8; DB 17; Length 788;
 Best Local Similarity 52.7%; Pred. No. 2.2e-08;
 Matches 147; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Db 346 AGTACATGCTGTGTAACGCTAGCAGACCAAGAACATCTACCAAGATCTACTACC 405
 357 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 416
 Oy 406 ACCGCCAAGGCTACTGCTACTGTCACCCACCAAGACAGTACCAAGACATCAACAGACA 465
 Db 417 ACT 476
 Oy 466 ACTACCAAGACTAGCACTACTGCGCTGCTTCTACTTCCACCTCTTCTGCTGCTTAC 525
 Db 477 ACT 536
 Oy 526 AAGGTATCTGCGGTAATCTGGCAGTGGTTCACAACCTCGTATTGGATTGTTGT 585
 Db 537 AGCTTATTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 596
 Oy 586 AAGCTTCTTGAGCGCTGGGAAAGCTTCTGCTACT 624
 Db 597 ACT 635

RESULT 14
 BH179321/c 627 bp DNA linear GSS 19-OCT-2001
 LOCUS 014_P_01-21 SMBAC1 Schistosoma mansoni genomic clone 014P01.5', DNA
 DEFINITION

ACCESSION BH179321
 VERSION BH179321.1
 KEYWORDS GI:16280048
 SOURCE GSS

ORGANISM Schistosoma mansoni.
 Schistosoma mansoni

REFERENCE
 AUTHORS Buktayova, Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeida; Schistosomatidae; Schistosomatidae; Schistosoma.
 Le Paslier, M.-C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Williams
 D.L., Johnston, D., Loverde, P.T. and Le Paslier, D.
 Construction and characterization of a Schistosoma mansoni
 bacterial artificial chromosome library
 Genomics 65 (2), 87-94 (2000)

TITLE
 JOURNAL MEDLINE
 COMMENT
 20247247
 Ocher GSSs: 014_P_01-rev
 Contact: Pierce RJ
 INSERM U 167
 Institut Pasteur de Lille
 1 rue du Professeur A. Calmette, 59019-Lille, France
 Tel: (33) (0)3 20877783
 Fax: (33) (0)3 20877888
 Email: Raymond.Pierce@pasteur-lille.fr
 CNS sequencing ID=D60AA014CH01CPI
 Plate: 014 row: P column: 01
 Seq primer: M13 -21 primer
 Class: BAC ends
 High quality sequence stop: 627.

FEATURES

Source

Location/Qualifiers

1. 627
 /organism="Schistosoma mansoni"
 /strain="Puerto-Rican"
 /db_xref="taxon:6183"
 /clone="014P01"
 /clone_lib="SMBAC1"
 /sex="mixed"
 /dev_stage="cercariae"
 /lab_host="Biomphalaria glabrata"
 /note="Vector: pBeloBAC 11; Site 1: Hind III; Partially
 Hind III digested and size-selected S. mansoni cercarial
 DNA was ligated into Hind III digested pBeloBAC 11 vector
 and used to transform E. coli DH10B. The complete library
 contains 23808 clones from 4 independent
 sizing-ligation-transformations. Average insert size
 ranges from 70-127 kb and genome coverage is 7.9-fold."
 16 others

BASE COUNT 169 a 79 c 196 g 167 t

ORIGIN

Query Match 5.8%; Score 67.2; DB 17; Length 627;
 Best Local Similarity 52.3%; Pred. No. 2.8e-08;
 Matches 135; Conservative 5; Mismatches 118; Indels 0; Gaps 0;

Oy 373 ACCAAGAGCATCTTACCAAGCATCTACCCGCGAAGGCTACTGCTACTGTCACC 432
 Db 398 AGGATTACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 492
 Oy 433 ACCAAGAGCATCTTACCAAGCATCTACCCGCGAAGGCTACTGCTACTGTCACC 492
 Db 338 ACTCTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 479
 Oy 493 GCTTCTACTGCACTCTTCTGCTGCTTCAAGGTCATCTCGGGGTAATCTGGC 552
 Db 278 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 612
 Oy 553 AGTGTTCACAACCTGATTGGATTGTTAAAGCTTCTGCGAGCTGGCGTGAAGA 612
 Db 218 ATTCTACTACACCTTCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 612
 Oy 613 GCTTCTGCTACTGCTGCT 630
 Db 158 AACCTGCTACTGCTACTACT 141

RESULT 15
 CNS07LFL/c 627 bp DNA linear GSS 08-OCT-2001
 LOCUS T7 end of clone 014CH01 of library SMBAC1 from strain Puerto-Rican
 DEFINITION

ACCESSION AL616275
 VERSION AL616275.1
 KEYWORDS GI:16029499
 SOURCE GSS

ORGANISM Schistosoma mansoni.
 Schistosoma mansoni
 Buktayova, Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeida; Schistosomatidae; Schistosomatidae; Schistosoma.
 Le Paslier, M.-C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Williams
 D.L., Johnston, D., Loverde, P.T. and Le Paslier, D.
 Construction and characterization of a Schistosoma mansoni
 bacterial artificial chromosome library
 Genomics 65 (2), 87-94 (2000)

TITLE
 JOURNAL MEDLINE
 COMMENT
 20247247
 10783255
 2 (bases 1 to 627)
 Genoscope.
 Direct Submision
 Submitted (05-OCT-2001) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 Partially Hind III digested and size-selected S. mansoni cercarial
 DNA was ligated into Hind III digested pBeloBAC 11 vector and used

REFERENCE
 AUTHORS Buktayova, Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeida; Schistosomatidae; Schistosomatidae; Schistosoma.
 Le Paslier, M.-C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Williams
 D.L., Johnston, D., Loverde, P.T. and Le Paslier, D.
 Construction and characterization of a Schistosoma mansoni
 bacterial artificial chromosome library
 Genomics 65 (2), 87-94 (2000)

TITLE
 JOURNAL MEDLINE
 COMMENT
 20247247
 10783255
 2 (bases 1 to 627)
 Genoscope.
 Direct Submision
 Submitted (05-OCT-2001) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 Partially Hind III digested and size-selected S. mansoni cercarial
 DNA was ligated into Hind III digested pBeloBAC 11 vector and used

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